

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101591,870A
Source: JFWO
Date Processed by STIC: 4/2/07

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 04/02/2007

PATENT APPLICATION: US/10/591,870A

TIME: 13:21:29

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04022007\J591870A.raw

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4 <110> APPLICANT: Lanahan, Mike
6 <120> TITLE OF INVENTION: Self-processing Plants and Plant Parts
8 <130> FILE REFERENCE: 109846.317
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,870A
C--> 10 <141> CURRENT FILING DATE: 2006-09-07
10 <150> PRIOR APPLICATION NUMBER: PCT/US04/07182
11 <151> PRIOR FILING DATE: 2004-03-15
13 <160> NUMBER OF SEQ ID NOS: 112
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 436
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: synthetic
25 <400> SEQUENCE: 1
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28 Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
29 20 25 30
30 Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
31 35 40 45
32 Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
33 50 55 60
34 Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
35 65 70 75 80
36 Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
37 85 90 95
38 Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
39 100 105 110
40 Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
41 115 120 125
42 Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
43 130 135 140
44 Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
45 145 150 155 160
46 Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
47 165 170 175
48 Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
49 180 185 190
50 Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
51 195 200 205
52 Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr

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53      210      215      220
54 Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
55 225      230      235      240
56 Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
57      245      250      255
58 Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
59      260      265      270
60 Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
61      275      280      285
62 His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
63      290      295      300
64 Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
65 305      310      315      320
66 Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
67      325      330      335
68 Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
69      340      345      350
70 Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
71      355      360      365
72 Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
73      370      375      380
74 Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
75 385      390      395      400
76 Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
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80 Cys Gly Val Gly
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85 <211> LENGTH: 1308
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: synthetic
92 <400> SEQUENCE: 2
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95 gccggcatct ccgcgatctg gataccgcca gcttccaagg gcatgtccgg gggctactcg 180
96 atgggctacg acccgtagca ctacttcgac ctccggcgagt actaccagaa gggcacggtg 240
97 gagacgcgct tcgggtccaa gcaggagctc atcaacatga tcaacacggc gcacgcctac 300
98 ggcatacaagg tcatcgcgga catcgtgatc aaccacaggg ccggcggcga cctggagtg 360
99 aaccggttcg tcggcgacta cacctggacg gactttctcca aggtcgcctc cggcaagtac 420
100 accgccaact acctcgactt ccacccaac gagctgcacg cgggcgactc cggcacgttc 480
101 ggcggtacc cggacatctg ccacgacaag tcctgggacc agtactggct ctgggcctcg 540
102 caggagtcct acgcggccta cctgcgctcc atcggcatcg acgcgtggcg cttcgactac 600
103 gtcaagggct acggggcctg ggtggtcaag gactggctca actggtgggg cggctggggc 660
104 gtgggcgagt actgggacac caacgtcgac gcgctgctca actgggccta ctccctccggc 720
105 gccaaagtg tgcacttccc cctgtactac aagatggacg cggccttcga caacaagaac 780

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106 atccccggcgc tcgtcgaggg cctgaagaac ggcgggcacgg tggctctccc cgacccggttc 840
107 aagggccgtga ccttcgtcgc caaccacgac acggacatca tctggaacaa gtacccggcg 900
108 tacgccttca tcctcaccta cgagggccag cccacgatct tctaccgca ctacgaggag 960
109 tggctgaaca aggacaagct caagaacctg atctggattc acgacaacct cgcgggcggc 1020
110 tccactagta tcgtgtacta cgactccgac gagatgatct tcgtccgcaa cggctacggc 1080
111 tccaagcccgc gcctgatcac gtacatcaac ctgggctcct ccaaggtggg ccgctgggtg 1140
112 tacgtcccga agttcgccgg cgctgcatc cagagtaca ccgcaacct cgcggtctgg 1200
113 gtggacaagt acgtgtactc ctccggctgg gtctacctgg agggcccggc ctacgacccc 1260
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118 <212> TYPE: PRT
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
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124 <400> SEQUENCE: 3
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127 Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met Asp Leu Thr
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129 Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala Lys Asp Val
130 35 40 45
131 Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
132 50 55 60
133 Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
134 65 70 75 80
135 Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val Ile Glu Ala
136 85 90 95
137 Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu Phe Lys Val
138 100 105 110
139 Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu Lys Ala Asp
140 115 120 125
141 Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
142 130 135 140
143 Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu Ile Ile Glu
144 145 150 155 160
145 Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu Asp Asp Tyr
146 165 170 175
147 Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu Lys Thr Ile
148 180 185 190
149 Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val Leu Leu Phe
150 195 200 205
151 Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn Met Glu Tyr
152 210 215 220
153 Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp Leu Asp Gly
154 225 230 235 240
155 Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile Arg Thr Thr
156 245 250 255
157 Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln Glu Ser Ala

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158          260          265          270
159 Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu Asn Asp Arg
160          275          280          285
161 Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His
162          290          295          300
163 Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys Asn Lys Gly
164 305          310          315          320
165 Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Gly Pro Gly Gly Val
166          325          330          335
167 Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr His Val His
168          340          345          350
169 Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu Asp Lys Asp
170          355          360          365
171 Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu Phe Met Val
172          370          375          380
173 Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His Thr Arg Ile
174 385          390          395          400
175 Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His Gly Ile Gly
176          405          410          415
177 Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile Gly Glu Leu
178          420          425          430
179 Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg Ile Asp Lys
180          435          440          445
181 Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val Ile Ala Ser
182          450          455          460
183 Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val Thr Tyr Trp
184 465          470          475          480
185 Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln Met Gly Leu
186          485          490          495
187 Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu His Lys Ile
188          500          505          510
189 Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly Trp Gly Ala
190          515          520          525
191 Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His Val Ala Ala
192          530          535          540
193 Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val Phe Asn Pro
194 545          550          555          560
195 Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu Thr Lys Ile
196          565          570          575
197 Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys Leu Ile Lys
198          580          585          590
199 Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala Ala Cys His
200          595          600          605
201 Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala Lys Ala Asp
202          610          615          620
203 Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala Gln Lys Leu
204 625          630          635          640
205 Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe Leu His Gly
206          645          650          655

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207 Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn Ser Tyr Asn
 208 660 665 670
 209 Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys Leu Gln Phe
 210 675 680 685
 211 Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu Arg Lys Glu
 212 690 695 700
 213 His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys Lys His Leu
 214 705 710 715 720
 215 Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met Leu Lys Asp
 216 725 730 735
 217 His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile Tyr Asn Gly
 218 740 745 750
 219 Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys Trp Asn Val
 220 755 760 765
 221 Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu Thr Val Glu
 222 770 775 780
 223 Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu Tyr Arg Glu
 224 785 790 795 800

227 <210> SEQ ID NO: 4

228 <211> LENGTH: 2400

229 <212> TYPE: DNA

230 <213> ORGANISM: Artificial Sequence

232 <220> FEATURE:

233 <223> OTHER INFORMATION: synthetic

235 <400> SEQUENCE: 4

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 238 aacgagtggc aggcgaagga cgtggccaag gaccgcttca tcgagatcaa ggacggcaag 180
 239 gccgaggtgt ggatactcca gggcgtggag gagatcttct acgagaagcc ggacacctcc 240
 240 ccgcgcacat tcttcgcccc ggcccgtccc aacaaggtga tcgaggcctt cctcaccaac 300
 241 ccggtggaca cctaagaaga ggagctgttc aaggtgaccg tcgacggcaa ggagatccc 360
 242 gtgtcccgcg tggagaaggc cgaccgcacc gacatcgacg tgaccaacta cgtgcgcac 420
 243 gtgctctccg agtccctcaa ggaggaggac ctccgcaagg acgtggagct gatcatcgag 480
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 245 gagctggggg cgggtgtactc cccggagaag accatcttcc gcgtgtggtc cccggtgtcc 600
 246 aagtgggtga aggtgtctct cttcaagaac ggcgaggaca ccgagccgta ccaggtgggtg 660
 247 aacatggagt acaagggcaa cggcgtgtgg gaggccgtgg tggagggcga cctcgacggc 720
 248 gtgttctacc tctaccagct ggagaactac ggcaagatcc gcaccaccgt ggacccgtac 780
 249 tccaaggccg tgtacgcaa caaccaggag tctgcagtgg tgaacctcgc ccgcaccaac 840
 250 ccggaggggt gggagaacga ccgcggcccg aagatcgagg gctacgagga cgccatcatc 900
 251 tacgagatcc acatcgccga catcaccggc ctggagaact ccggcgtgaa gaacaagggc 960
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 253 tcccacctcg tggagctggg cgtgaccac gtgcacatcc tcccgttctt cgacttctac 1080
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 258 tactacttct accgcatcga caagaccggc gcctacctca acgagtccgg ctgcggcaac 1380
 259 gtgatcgcc ccgagcgccc gatgatgcgc aagttcatcg tggacaccgt gacctactgg 1440

VERIFICATION SUMMARY

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Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04022007\J591870A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3247 M:283 W: Missing Blank Line separator, <220> field identifier